

SEQUENCE LISTING

- (1) GENERAL INFORMATION:
- (i) APPLICANT: SCHENDEL, Dolores J.
 - (ii) TITLE OF INVENTION: T CELLS SPECIFIC FOR KIDNEY CARCINOMA
 - (iii) NUMBER OF SEQUENCES: 54
 - (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Arent Fox Kintner Plotkin & Kahn
 - (B) STREET: 1050 Connecticut Avenue, Suite 400
 - (C) CITY: Washington
 - (D) STATE: DC
 - (E) COUNTRY: USA
 - (F) ZIP: 20036-5339
 - (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
 - (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/881,509
 - (B) FILING DATE: June 24, 1997
 - (C) CLASSIFICATION:
 - (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Kitts, Monica Chin
 - (B) REGISTRATION NUMBER: 36,105
 - (C) REFERENCE/DOCKET NUMBER: 100564-07015
 - (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (202) 857-6000
 - (B) TELEFAX: (202) 638-4810
- (2) INFORMATION FOR SEQ ID NO: 1:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1341 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION:1..801
 - (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: 1...54

(ix) FEATURE:

(A) (B) NAME/KEY: mat_peptide LOCATION:55..801

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

AT Me -1		G CA g Gl	A GT n Va -1	T VT	G AG a Ar	A GTO	G AT	C GT e Va -1	I Ph	C CI e Le	'G AC	CC C	TG A	AGT Ser -5	ACT Thr	TTG Leu	48
AG Se	C CT r Le	α 11 <u>1</u>	T AAG a Ly: 1	G AC	C ACC	C CAG c Glr 5	Pro	C ATO	C TCO	C AT r Me	t As	C TO	CA T	AT 'yr	GAA Glu	GGA Gly	96
CAZ Gli 15	01	A GT ı Va	G AA(l Asr	C ATA	A ACC Thr 20	. cys	AGC Ser	CAC His	C AA(s Asr	C AA n As: 2	n Il	T GO e Al	CT A	CA hr	AAT Asn	GAT Asp 30	144
TAT Tyr	T ATO	C ACC	G TGO	TAC Tyr 35	. GIII	CAG Gln	TTI Phe	CCC Pro	AGC Ser 40	Gli	A GG n Gl	A CC y Pr	CA C	GA rg	TTT Phe 45	ATT Ile	192
ATT Ile	CA/	A GGA	A TAC 7 Tyr 50	пys	G ACA	AAA Lys	GTT Val	ACA Thr 55	Asn	GAZ Glu	A GTO	G GC l Al	a S	CC er 60	CTG Leu	TTT Phe	240
ATC Ile	CCT Pro	GCC Ala	GAC Asp	AGA Arg	AAG Lys	TCC Ser	AGC Ser 70	Thr	CTG Leu	AG(Ser	CTC Leu	G CC 1 Pr	0 A:	GG rg	GTT Val	TCC Ser	288
CTG Leu	AGC Ser 80	GAC Asp	ACT Thr	GCT Ala	GTG Val	TAC Tyr 85	TAC Tyr	TGC Cys	CTC Leu	GTG Val	GGT Gly 90	' Gl	T TO y Se	CT (er <i>l</i>	GCA Ala	AGG Arg	336
CAA Gln 95	CTG Leu	ACC Thr	TTT Phe	GGA Gly	TCT Ser 100	GGG Gly	ACA Thr	CAA Gln	TTG Leu	ACT Thr 105	GTT Val	TT <i>I</i> Let	A CC	CT (GAT Asp	ATC Ile 110	384
CAG Gln	AAC Asn	CCT Pro	GAC Asp	CCT Pro 115	GCC Ala	GTG Val	TAC Tyr	CAG Gln	CTG Leu 120	AGA Arg	GAC Asp	TCI Ser	C AA	s S	CCC Ser .25	AGT Ser	432
GAC Asp	AAG Lys	TCT Ser	GTC Val 130	TGC Cys	CTA Leu	TTC Phe	Thr	GAT Asp 135	TTT Phe	GAT Asp	TCT Ser	CAA Gln	AC Th	r A	AT sn	GTG Val	480
TCA Ser	CAA Gln	AGT Ser 145	AAG Lys	GAT Asp	TCT Ser	Asp	GTG Val 150	TAT Tyr	ATC Ile	ACA Thr	GAC Asp	AAA Lys 155	AC'	T G r V	TG (CTA Leu	528
-100	ATG Met 160	AGG Arg	TCT Ser	ATG Met	ASP	TTC <i>1</i> Phe 1 165	AAG . Lys :	AGC . Ser .	AAC . Asn	AGT Ser	GCT Ala 170	GTG Val	GC0 Ala	C T(GG A	AGC Ser	576
AAC . Asn	AAA Lys	TCT Ser	GAC Asp	TTT (GCA '	TGT (Cys <i>F</i>	SCA A	AAC (Asn A	GCC '	TTC Phe	AAC Asn	AAC Asn	AGC Ser	C A	rr A le I	TT le	624

175 180 185 190	•
CCA GAA GAC ACC TTC TTC CCC AGC CCA GAA AGT TCC TGT GAT GTC AAG Pro Glu Asp Thr Phe Phe Pro Ser Pro Glu Ser Ser Cys Asp Val Lys 195 200 205	672
CTG GTC GAG AAA AGC TTT GAA ACA GAT ACG AAC CTA AAC TTT CAA AAC Leu Val Glu Lys Ser Phe Glu Thr Asp Thr Asn Leu Asn Phe Gln Asn 210 220	720
CTG TCA GTG ATT GGG TTC CGA ATC CTC CTC CTG AAA GTG GCC GGG TTT Leu Ser Val Ile Gly Phe Arg Ile Leu Leu Leu Lys Val Ala Gly Phe 225 230 235	768
AAT CTG CTC ATG ACG CTG CGG CTG TGG TCC AGC TGAGATCTGC AAGATTGTAA Asn Leu Leu Met Thr Leu Arg Leu Trp Ser Ser 240 245	821
GACAGCCTGT GCTCCCTCGC TCCTTCCTCT GCATTGCCCC TCTTCTCCCT CTCCAAACAG	881
AGGGAACTCT CCTACCCCCA AGGAGGTGAA AGCTGCTACC ACCTCTGTGC CCCCCCGGCA	941
ATGCCACCAA CTGGATCCTA CCCGAATTTA TGATTAAGAT TGCTGAAGAG CTGCCAAACA	1001
CTGCTGCCAC CCCCTCTGTT CCCTTATTGC TGCTTGTCAC TGCCTGACAT TCACGGCAGA	1061
GGCAAGGCTG CTGCAGCCTC CCCTGGCTGT GCACATTCCC TCCTGCTCCC CAGAGACTGC	1121
CTCCGCCATC CCACAGATGA TGGATCTTCA GTGGGTTCTC TTGGGCTCTA GGTCCTGGAG	1181
AATGTTGTGA GGGGTTTATT TTTTTTTAAT AGTGTTCATA AAGAAATACA TAGTATTCTT	1241
CTTCTCAAGA CGTGGGGGA AATTATCTCA TTATCGAGGC CCTGCTATGC TGTGTGTCTG	1301
GGCGTGTTGT ATGTCCTGCT GCCGATGCCT TCATTAAAAT	1341
(2) INFORMATION FOR SEQ ID NO: 2:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 267 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear	
<pre>(ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:</pre>	
Met Arg Gln Val Ala Arg Val Ile Val Phe Leu Thr Leu Ser Thr Leu -18 -15 -5	
Ser Leu Ala Lys Thr Thr Gln Pro Ile Ser Met Asp Ser Tyr Glu Gly 1 5 10	
Gln Glu Val Asn Ile Thr Cys Ser His Asn Asn Ile Ala Thr Asn Asp 15 20 25 30	

Tyr Ile Thr Trp Tyr Gln Gln Phe Pro Ser Gln Gly Pro Arg Phe Ile

35 40 45

Ile Gln Gly Tyr Lys Thr Lys Val Thr Asn Glu Val Ala Ser Leu Phe 50 55 60

Ile Pro Ala Asp Arg Lys Ser Ser Thr Leu Ser Leu Pro Arg Val Ser 65 70 75

Leu Ser Asp Thr Ala Val Tyr Tyr Cys Leu Val Gly Gly Ser Ala Arg 80 85 90

Gln Leu Thr Phe Gly Ser Gly Thr Gln Leu Thr Val Leu Pro Asp Ile 95 100 105 110

Gln Asn Pro Asp Pro Ala Val Tyr Gln Leu Arg Asp Ser Lys Ser Ser 115 120 125

Asp Lys Ser Val Cys Leu Phe Thr Asp Phe Asp Ser Gln Thr Asn Val

Ser Gln Ser Lys Asp Ser Asp Val Tyr Ile Thr Asp Lys Thr Val Leu 145 150 155

Asp Met Arg Ser Met Asp Phe Lys Ser Asn Ser Ala Val Ala Trp Ser 160 165 170

Asn Lys Ser Asp Phe Ala Cys Ala Asn Ala Phe Asn Asn Ser Ile Ile 175 180 185 190

Pro Glu Asp Thr Phe Phe Pro Ser Pro Glu Ser Ser Cys Asp Val Lys 195 200 205

Leu Val Glu Lys Ser Phe Glu Thr Asp Thr Asn Leu Asn Phe Gln Asn 210 215 220

Leu Ser Val Ile Gly Phe Arg Ile Leu Leu Leu Lys Val Ala Gly Phe 225 230 235

Asn Leu Leu Met Thr Leu Arg Leu Trp Ser Ser 240 245

(2) INFORMATION FOR SEQ ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 936 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear
 - (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1...933
 - (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide
 - (B) LOCATION: 1..63

(ix) FEATURE:

(A) NAME/KEY: mat_peptide(B) LOCATION: 64..933

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

Met	GAT Asp -20	Thr	TGG Trp	CTC Leu	GTA Val	TGC Cys -15	Trp	GCA Ala	ATT Ile	TTT Phe	AGT Ser -10	Leu	TTG Leu	AAA Lys	GCA Ala	48
GGA Gly -5	Leu	ACA Thr	GAA Glu	CCT Pro	GAA Glu 1	Val	ACC Thr	CAG Gln	ACT Thr 5	CCC Pro	AGC Ser	CAT His	CAG Gln	GTC Val 10	ACA Thr	96
CAG Gln	ATG Met	GGA Gly	CAG Gln 15	GAA Glu	GTG Val	ATC Ile	TTG Leu	CGC Arg 20	TGT Cys	GTC Val	CCC Pro	ATC Ile	TCT Ser 25	AAT Asn	CAC His	144
TTA Leu	TAC Tyr	TTC Phe 30	Tyr	TGG Trp	TAC Tyr	AGA Arg	CAA Gln 35	ATC Ile	TTG Leu	GGG Gly	CAG Gln	AAA Lys 40	GTC Val	GAG Glu	TTT Phe	192
CTG Leu	GTT Val 45	TCC Ser	TTT Phe	TAT Tyr	AAT Asn	AAT Asn 50	GAA Glu	ATC Ile	TCA Ser	GAG Glu	AAG Lys 55	TCT Ser	GAA Glu	ATA Ile	TTC Phe	240
GAT Asp 60	GAT Asp	CAA Gln	TTC Phe	TCA Ser	GTT Val 65	GAA Glu	AGG Arg	CCT Pro	GAT Asp	GGA Gly 70	TCA Ser	AAT Asn	TTC Phe	ACT Thr	CTG Leu 75	288
AAG Lys	ATC Ile	CGG Arg	TCC Ser	ACA Thr 80	AAG Lys	CTG Leu	GAG Glu	GAC Asp	TCA Ser 85	GCC Ala	ATG Met	TAC Tyr	TTC Phe	TGT Cys 90	GCC Ala	336
AGC Ser	AGC Ser	GAA Glu	ACT Thr 95	AAC Asn	TCC Ser	TAC Tyr	GAG Glu	CAG Gln 100	TAC Tyr	TTC Phe	GGG Gly	CCG Pro	GGC Gly 105	ACC Thr	AGG Arg	384
CTC Leu	ACG Thr	GTC Val 110	ACA Thr	GAG Glu	GAC Asp	CTG Leu	AAA Lys 115	AAC Asn	GTG Val	TTC Phe	CCA Pro	CCC Pro 120	GAG Glu	GTC Val	GCT Ala	432
GTG Val	TTT Phe 125	GAG Glu	CCA Pro	TCA Ser	GAA Glu	GCA Ala 130	GAG Glu	ATC Ile	TCC Ser	CAC His	ACC Thr 135	CAA Gln	AAG Lys	GCC Ala	ACA Thr	480
CTG Leu 140	GTG Val	TGC Cys	CTG Leu	GCC Ala	ACA Thr 145	GGC Gly	TTC Phe	TAC Tyr	CCC Pro	GAC Asp 150	CAC His	GTG Val	GAG Glu	CTG Leu	AGC Ser 155	528
TGG Trp	TGG Trp	GTG Val	AAT Asn	GGG Gly 160	AAG Lys	GAG Glu	GTG Val	His	AGT Ser 165	GGG Gly	GTC Val	AGC Ser	ACA Thr	GAC Asp 170	CCG Pro	576
CAG Gln	CCC Pro	CTC Leu	AAG Lys	GAG Glu	CAG Gln	CCC Pro	GCC Ala	CTC Leu	AAT Asn	GAC Asp	TCC Ser	AGA Arg	TAC Tyr	TGC Cys	CTG Leu	624

175 180 185 AGC AGC CGC CTG AGG GTC TCG GCC ACC TTC TGG CAG AAC CCC CGC AAC 672 Ser Ser Arg Leu Arg Val Ser Ala Thr Phe Trp Gln Asn Pro Arg Asn 190 195 CAC TTC CGC TGT CAA GTC CAG TTC TAC GGG CTC TCG GAG AAT GAC GAG 720 His Phe Arg Cys Gln Val Gln Phe Tyr Gly Leu Ser Glu Asn Asp Glu 210 TGG ACC CAG GAT AGG GCC AAA CCT GTC ACC CAG ATC GTC AGC GCC GAG 768 Trp Thr Gln Asp Arg Ala Lys Pro Val Thr Gln Ile Val Ser Ala Glu 235 GCC TGG GGT AGA GCA GAC TGT GGC TTC ACC TCC GAG TCT TAC CAG CAA 816 Ala Trp Gly Arg Ala Asp Cys Gly Phe Thr Ser Glu Ser Tyr Gln Gln 240 GGG GTC CTG TCT GCC ACC ATC CTC TAT GAG ATC TTG CTA GGG AAG GCC 864 Gly Val Leu Ser Ala Thr Ile Leu Tyr Glu Ile Leu Leu Gly Lys Ala 255 ACC TTG TAT GCC GTG CTG GTC AGT GCC CTC GTG CTG ATG GCC ATG GTC 912 Thr Leu Tyr Ala Val Leu Val Ser Ala Leu Val Leu Met Ala Met Val 270 275 280 AAG AGA AAG GAT TCC AGA GGC TAG 936 Lys Arg Lys Asp Ser Arg Gly 285 (2) INFORMATION FOR SEQ ID NO: 4: (i) SEQUENCE CHARACTERISTICS: LENGTH: 311 amino acids (A) (B) TYPE: amino acid (D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4: Met Asp Thr Trp Leu Val Cys Trp Ala Ile Phe Ser Leu Leu Lys Ala Gly Leu Thr Glu Pro Glu Val Thr Gln Thr Pro Ser His Gln Val Thr Gln Met Gly Gln Glu Val Ile Leu Arg Cys Val Pro Ile Ser Asn His 15 Leu Tyr Phe Tyr Trp Tyr Arg Gln Ile Leu Gly Gln Lys Val Glu Phe Leu Val Ser Phe Tyr Asn Asn Glu Ile Ser Glu Lys Ser Glu Ile Phe 45 55 Asp Asp Gln Phe Ser Val Glu Arg Pro Asp Gly Ser Asn Phe Thr Leu

65

60

70

75

Lys	Ile	Arg	Ser	Thr 80	Lys	Leu	Glu	Asp	Ser 85	Ala	Met	Tyr	Phe	Cys 90	Ala
Ser	Ser	Glu	Thr 95	Asn	Ser	Tyr	Glu	Gln 100	Tyr	Phe	Gly	Pro	Gly 105	Thr	Arg
Leu	Thr	Val 110	Thr	Glu	Asp	Leu	Lys 115	Asn	Val	Phe	Pro	Pro 120	Glu	Val	Ala
Val	Phe 125	Glu	Pro	Ser	Glu	Ala 130	Glu	Ile	Ser	His	Thr 135	Gln	Lys	Ala	Thr
Leu 140	Val	Суѕ	Leu	Ala	Thr 145	Gly	Phe	Tyr	Pro	Asp 150	His	Val	Glu	Leu	Ser 155
Trp	Trp	Val	Asn	Gly 160	Lys	Glu	Val	His	Ser 165	Gly	Val	Ser	Thr	Asp 170	Pro
Gln	Pro	Leu	Lys 175	Glu	Gln	Pro	Ala	Leu 180	Asn	Asp	Ser	Arg	Tyr 185	Cys	Leu
Ser	Ser	Arg 190	Leu	Arg	Val	Ser	Ala 195	Thr	Phe	Trp	Gln	Asn 200	Pro	Arg	Asn
His	Phe 205	Arg	Суѕ	Gln	Val	Gln 210	Phe	Tyr	Gly	Leu	Ser 215	Glu	Asn	Asp	Glu
Trp 220	Thr	Gln	Asp	Arg	Ala 225	Lys	Pro	Val	Thr	Gln 230	Ile	Val	Ser	Ala	Glu 235
Ala	Trp	Gly	Arg	Ala 240	Asp	Cys	Gly	Phe	Thr 245	Ser	Glu	Ser	Tyr	Gln 250	Gln
Gly	Val	Leu	Ser 255	Ala	Thr	Ile	Leu	Tyr 260	Glu	Ile	Leu	Leu	Gly 265	Lys	Ala
Thr	Leu	Tyr 270	Ala	Val	Leu	Val	Ser 275	Ala	Leu	Val	Leu	Met 280	Ala	Met	Val
Lys	Arg 285	Lys	Asp	Ser	Arg	Gly 290									
(2)	INFC	RMAT	CION	FOR	SEQ	ID N	10: 5	:							
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 39 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: both (D) TOPOLOGY: linear														
	(ix		EATU N		KEY•	CDS									

(B) LOCATION:1..39

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

TGC CTC GTC CTT TCT GGT TCT GCA AGG CAA CTG ACC TTT 39 Cys Leu Val Leu Ser Gly Ser Ala Arg Gln Leu Thr Phe 295 300 (2) INFORMATION FOR SEQ ID NO: 6: (i) SEQUENCE CHARACTERISTICS: LENGTH: 13 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6: Cys Leu Val Leu Ser Gly Ser Ala Arg Gln Leu Thr Phe 5 10 (2) INFORMATION FOR SEQ ID NO: 7: (i) SEQUENCE CHARACTERISTICS: LENGTH: 36 base pairs TYPE: nucleic acid (B) (C) STRANDEDNESS: both (D) TOPOLOGY: linear (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION:1..36 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7: TGC CTC GCT ACT GGT TCT GCA AGG CAA CTG ACC TTT 36 Cys Leu Ala Thr Gly Ser Ala Arg Gln Leu Thr Phe 15 20 25 (2) INFORMATION FOR SEQ ID NO: 8: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 12 amino acids (B) TYPE: amino acid TOPOLOGY: linear (D) (ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8: Cys Leu Ala Thr Gly Ser Ala Arg Gln Leu Thr Phe 1 5 (2) INFORMATION FOR SEQ ID NO: 9:

(i)

SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 base pairs

	(B) TYPE: nucleic acid(C) STRANDEDNESS: both(D) TOPOLOGY: linear	
	(ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION:139	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:	
TGT Cys	GCC AGC AGT GGA ACA GAT TCC TAC GAG CAG TAC TTC Ala Ser Ser Gly Thr Asp Ser Tyr Glu Gln Tyr Phe 15 20 25	39
(2)	INFORMATION FOR SEQ ID NO: 10:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 13 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:	
Cys 1	Ala Ser Ser Gly Thr Asp Ser Tyr Glu Gln Tyr Phe 5 10	
(2)	INFORMATION FOR SEQ ID NO: 11:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 39 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: both (D) TOPOLOGY: linear	
	(ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION:139	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:	
TGT Cys	GCC AGC AGT GAA ACA GAT TCC TAC GAG CAG TAC TTC Ala Ser Ser Glu Thr Asp Ser Tyr Glu Gln Tyr Phe 15 20 25	39
(2)	INFORMATION FOR SEQ ID NO: 12:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 13 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear	
	<pre>(ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:</pre>	

Cys 1	5 10	
(2)	INFORMATION FOR SEQ ID NO: 13:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 39 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: both (D) TOPOLOGY: linear	
	(ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION:139	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:	
	GCC AGC AGT GGA ACA GCT TCC TAC GAG CAG TAC TTC Ala Ser Ser Gly Thr Ala Ser Tyr Glu Gln Tyr Phe 15 20 25	39
(2)	INFORMATION FOR SEQ ID NO: 14:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 13 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:	
Cys 1	Ala Ser Ser Gly Thr Ala Ser Tyr Glu Gln Tyr Phe 5 10	
(2)	INFORMATION FOR SEQ ID NO: 15:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 39 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: both (D) TOPOLOGY: linear	
	(ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION:139	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:	
	GCC AGC AGT GGT ACA AAC TCC TAC GAG CAG TAC TTT Ala Ser Ser Gly Thr Asn Ser Tyr Glu Gln Tyr Phe 15 20 25	39
(2)	INFORMATION FOR SEQ ID NO: 16:	

(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 13 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear
	(ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:
Cys 1	Ala Ser Ser Gly Thr Asn Ser Tyr Glu Gln Tyr Phe 5 10
(2)	INFORMATION FOR SEQ ID NO: 17:
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 39 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: both (D) TOPOLOGY: linear
	<pre>(ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION:139</pre>
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:
	GCC ACC TCC GGG ACA GCT TCC TAC GAG CAG TAC TTC Ala Thr Ser Gly Thr Ala Ser Tyr Glu Gln Tyr Phe 15 20 25
(2)	INFORMATION FOR SEQ ID NO: 18:
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 13 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:
Cys 1	Ala Thr Ser Gly Thr Ala Ser Tyr Glu Gln Tyr Phe 5 10
(2)	INFORMATION FOR SEQ ID NO: 19:
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 39 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: both (D) TOPOLOGY: linear
	(ix) FEATURE:

(A) NAME/KEY: CDS

LOCATION:1..39

(B)

39

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:	
TGT Cys	GCC AGA TCC GGG ACA GGC TCC TAC GAG CAG TAC TTC Ala Arg Ser Gly Thr Gly Ser Tyr Glu Gln Tyr Phe 15 20 25	39
(2)	INFORMATION FOR SEQ ID NO: 20:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 13 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:	
Cys 1	Ala Arg Ser Gly Thr Gly Ser Tyr Glu Gln Tyr Phe 5 10	
(2)	INFORMATION FOR SEQ ID NO: 21:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:	
CACI	GAAGAT CCATCATCTG	20
(2)	INFORMATION FOR SEQ ID NO: 22:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:	
TAGA	AGGATGG TGGCAGACAG	20
(2)	INFORMATION FOR SEQ ID NO:23:	
	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 15 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: not relevant (D) TOPOLOGY: not relevant 	

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Tyr Cys Leu Xaa Xaa Xaa Xaa Ser Ala Arg Gln Leu Thr Phe 1 5 10 15

- (2) INFORMATION FOR SEQ ID NO:24:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: not relevant
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Cys Ala Xaa Xaa Xaa Xaa Xaa Xaa Xaa Tyr Glu Gln Tyr Phe $1 \hspace{1.5cm} 5 \hspace{1.5cm} 10$

- (2) INFORMATION FOR SEQ ID NO:25:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: not relevant
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Cys Ala Xaa Xaa Xaa Xaa Xaa Xaa Asn Glu Gln Phe Phe 1 5 10

- (2) INFORMATION FOR SEQ ID NO:26:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: not relevant
 - (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Cys Ala Xaa Xaa Xaa Xaa Xaa Xaa Asp Thr Gln Tyr Phe 1 5 10

- (2) INFORMATION FOR SEQ ID NO:27:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: not relevant
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Ser Ser Glu Thr Asn Ser 1 5

- (2) INFORMATION FOR SEQ ID NO:28:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: not relevant
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Ser Ser Glu Thr Ser Ser 1 5

- (2) INFORMATION FOR SEQ ID NO:29:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: not relevant
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Thr Ser Gly Thr Ala Ser

- (2) INFORMATION FOR SEQ ID NO:30:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: not relevant
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Arg Ser Gly Thr Gly Ser 1 5

- (2) INFORMATION FOR SEQ ID NO:31:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: not relevant
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Ser Ser Gly Thr Asp Ser 1 5

- (2) INFORMATION FOR SEQ ID NO:32:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: not relevant
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Ser Ser Gly Thr Arg Ser

- (2) INFORMATION FOR SEQ ID NO:33:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: not relevant
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Ser Ser Gly Ser Asp Ser 1 5

- (2) INFORMATION FOR SEQ ID NO:34:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: not relevant
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Ser Ser Ser Thr Gly Ser 1 5

- (2) INFORMATION FOR SEQ ID NO:35:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: not relevant
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEO ID NO:35:

Ser Ser Ser Thr Val Ser 1 5

- (2) INFORMATION FOR SEQ ID NO:36:
 - (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6 amino acids

(B) TYPE: amino acid

- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Ser Ser Ser Thr Leu Ser 1 5

- (2) INFORMATION FOR SEO ID NO:37:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: not relevant
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Ser Ser Ser Thr Leu Phe 1 5

- (2) INFORMATION FOR SEQ ID NO:38:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: not relevant
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Ser Ser Ser Thr Ala Ser 1 5

- (2) INFORMATION FOR SEQ ID NO:39:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant

(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Ser Ser His Thr Asp Ser 1 5

- (2) INFORMATION FOR SEQ ID NO:40:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: not relevant
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Ser Ser Asp Thr Leu Ser 1 5

- (2) INFORMATION FOR SEQ ID NO:41:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: not relevant
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Ser Arg Trp Asp Ser Glu 1 5

- (2) INFORMATION FOR SEQ ID NO:42:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Ser Ser Gly Thr Ser Ser Tyr 1 5

- (2) INFORMATION FOR SEQ ID NO:43:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: not relevant
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Ser Ser Asp Gln Gly Met
1 5

- (2) INFORMATION FOR SEQ ID NO:44:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: not relevant
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Ser Ala Asp Ser Phe Lys 1 5

- (2) INFORMATION FOR SEQ ID NO: 45:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 base pairs
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide (ix) FEATURE: (A) NAME/KEY: misc feature LOCATION:2..9 (B) (C) OTHER INFORMATION: /note= "Xaa(1) to Xaa(7) represents a sequence of 5 to 7 amino acids (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45: Cys Ala Xaa Xaa Xaa Xaa Xaa Xaa Asp Glu Gln Tyr Phe (2) INFORMATION FOR SEQ ID NO:46: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 13 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: not relevant (D) TOPOLOGY: not relevant (ii) MOLECULE TYPE: peptide (xi) SEQUENCE DESCRIPTION: SEQ ID NO:46: Tyr Cys Leu Val Gly Gly Ser Ala Arg Gln Leu Thr Phe 15 (2) INFORMATION FOR SEQ ID NO: 47: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 14 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: not relevant (D) TOPOLOGY: not relevant (ii) MOLECULE TYPE: peptide (xi) SEQUENCE DESCRIPTION: SEQ ID NO:47: Tyr Cys Leu Val Leu Ser Gly Ser Ala Arg Gln Leu Thr Phe 10 (2) INFORMATION FOR SEQ ID NO:48: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 13 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: not relevant (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

	Tyr Cys Leu Ala Thr Gly Ser Ala Arg Gln Leu Thr Phe 1 5 10	15
(2)	INFORMATION FOR SEQ ID NO:49:	
	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 13 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: not relevant (D) TOPOLOGY: not relevant 	
	(ii) MOLECULE TYPE: peptide	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:	
	Tyr Cys Leu Val Ser Gly Ser Ala Arg Gln Leu Thr Phe 1 5 10	15
(2)	INFORMATION FOR SEQ ID NO:50:	
	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 13 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: not relevant (D) TOPOLOGY: not relevant 	
	(ii) MOLECULE TYPE: peptide	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:	
	Tyr Cys Leu Asp Ser Gly Ser Ala Arg Gln Leu Thr Phe 1 5 10	15
(2)	INFORMATION FOR SEQ ID NO:51:	
	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 14 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: not relevant (D) TOPOLOGY: not relevant 	
	(ii) MOLECULE TYPE: peptide	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:	
	Tyr Cys Leu Val Val Ser Gly Ser Ala Arg Gln Leu Thr Phe 1 5 10	15
(2)	INFORMATION FOR SEQ ID NO:52:	

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14 amino acids

(C) STRANDEDNESS: not relevant (D) TOPOLOGY: not relevant (ii) MOLECULE TYPE: peptide (xi) SEQUENCE DESCRIPTION: SEQ ID NO:52: Tyr Cys Leu Ala Leu Ala Gly Ser Ala Arg Gln Leu Thr Phe 15 (2) INFORMATION FOR SEQ ID NO:53: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 14 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: not relevant (D) TOPOLOGY: not relevant (ii) MOLECULE TYPE: peptide (xi) SEQUENCE DESCRIPTION: SEQ ID NO:53: Tyr Cys Leu Ala Pro Ser Gly Ser Ala Arg Gln Leu Thr Phe 15 (2) INFORMATION FOR SEQ ID NO:54: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 13 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: not relevant (D) TOPOLOGY: not relevant (ii) MOLECULE TYPE: peptide (xi) SEQUENCE DESCRIPTION: SEQ ID NO:54: Tyr Cys Leu Val Gly Arg Ser Ala Arg Gln Leu Thr Phe 15

(B) TYPE: amino acid